SEQUENCE LISTING

<110> Takeda Pharmaceutical Company Limited

<120> Novel Screening Method

<130> G05-0036

<150> JP 2003-010001
<151> 2003-01-17

<150> JP 2003-104540
<151> 2003-04-08

<150> JP 2003-194497
<151> 2003-07-09

<150> JP 2003-329080
<151> 2003-09-19

<150> PCT/JP2004/000248
<151> 2004-01-15

<160> 22

<210> 1
<211> 361
<212> PRT
<213> Homo sapiens

<400> 1
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Leu Glu Gln Ala Asn Arg Thr Arg Phe Pro Phe Phe Ser Asp Val Lys
            20                  25                  30
Gly Asp His Arg Leu Val Leu Ala Ala Val Glu Thr Thr Val Leu Val
        35                  40                  45
Leu Ile Phe Ala Val Ser Leu Leu Gly Asn Val Cys Ala Leu Val Leu
    50                  55                  60
Val Ala Arg Arg Arg Arg Arg Gly Ala Thr Ala Cys Leu Val Leu Asn
65                  70                  75                  80
Leu Phe Cys Ala Asp Leu Leu Phe Ile Ser Ala Ile Pro Leu Val Leu
                85                  90                  95
Ala Val Arg Trp Thr Glu Ala Trp Leu Leu Gly Pro Val Ala Cys His
            100                 105                 110
Leu Leu Phe Tyr Val Met Thr Leu Ser Gly Ser Val Thr Ile Leu Thr
        115                 120                 125
Leu Ala Ala Val Ser Leu Glu Arg Met Val Cys Ile Val His Leu Gln
    130                 135                 140
Arg Gly Val Arg Gly Pro Gly Arg Arg Ala Arg Ala Val Leu Leu Ala
145                 150                 155                 160
Leu Ile Trp Gly Tyr Ser Ala Val Ala Ala Leu Pro Leu Cys Val Phe
                165                 170                 175
Phe Arg Val Val Pro Gln Arg Leu Pro Gly Ala Asp Gln Glu Ile Ser
            180                 185                 190
Ile Cys Thr Leu Ile Trp Pro Thr Ile Pro Gly Glu Ile Ser Trp Asp
        195                 200                 205
Val Ser Phe Val Thr Leu Asn Phe Leu Val Pro Gly Leu Val Ile Val
    210                 215                 220
Ile Ser Tyr Ser Lys Ile Leu Gln Ile Thr Lys Ala Ser Arg Lys Arg
225                 230                 235                 240
Leu Thr Val Ser Leu Ala Tyr Ser Glu Ser His Gln Ile Arg Val Ser
                245                 250                 255
Gln Gln Asp Phe Arg Leu Phe Arg Thr Leu Phe Leu Leu Met Val Ser
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            260                 265                 270
Phe Phe Ile Met Trp Ser Pro Ile Ile Ile Thr Ile Leu Leu Ile Leu
        275                 280                 285
Ile Gln Asn Phe Lys Gln Asp Leu Val Ile Trp Pro Ser Leu Phe Phe
    290                 295                 300
Trp Val Val Ala Phe Thr Phe Ala Asn Ser Ala Leu Asn Pro Ile Leu
305                 310                 315                 320
Tyr Asn Met Thr Leu Cys Arg Asn Glu Trp Lys Lys Ile Phe Cys Cys
                325                 330                 335
Phe Trp Phe Pro Glu Lys Gly Ala Ile Leu Thr Asp Thr Ser Val Lys
            340                 345                 350
Arg Asn Asp Leu Ser Ile Ile Ser Gly
        355                 360

<210> 2
<211> 1083
<212> DNA
<213> Homo sapiens

<400> 2
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aaccgcaccc gctttccctt cttctccgac gtcaagggcg accaccggct ggtgctggcc  120
gcggtggaga caaccgtgct ggtgctcatc tttgcagtgt cgctgctggg caacgtgtgc  180
gccctggtgc tggtggcgcg ccgacgacgc cgcggcgcga ctgcctgcct ggtactcaac  240
ctcttctgcg cggacctgct cttcatcagc gctatccctc tggtgctggc cgtgcgctgg  300
actgaggcct ggctgctggg ccccgttgcc tgccacctgc tcttctacgt gatgaccctg  360
agcggcagcg tcaccatcct cacgctggcc gcggtcagcc tggagcgcat ggtgtgcatc  420
gtgcacctgc agcgcggcgt gcggggtcct gggcggcggg cgcgggcagt gctgctggcg  480
ctcatctggg gctattcggc ggtcgccgct ctgcctctct gcgtcttctt ccgagtcgtc  540
ccgcaacggc tccccggcgc cgaccaggaa atttcgattt gcacactgat ttggcccacc  600
attcctggag agatctcgtg ggatgtctct tttgttactt tgaacttctt ggtgccagga  660
ctggtcattg tgatcagtta ctccaaaatt ttacagatca caaaggcatc aaggaagagg  720
ctcacggtaa gcctggccta ctcggagagc caccagatcc gcgtgtccca gcaggacttc  780
cggctcttcc gcaccctctt cctcctcatg gtctccttct tcatcatgtg gagccccatc  840
atcatcacca tcctcctcat cctgatccag aacttcaagc aagacctggt catctggccg  900
tccctcttct tctgggtggt ggccttcaca tttgctaatt cagcccctaaa ccccatcctc  960
tacaacatga cactgtgcag gaatgagtgg aagaaaattt tttgctgctt ctggttccca 1020
gaaaagggag ccattttaac agacacatct gtcaaaagaa atgacttgtc gattatttct 1080
ggc                                                               1083

<210> 3
<211> 361
<212> PRT
<213> Mus musculus

<400> 3
Met Ser Pro Glu Cys Ala Gln Thr Thr Gly Pro Gly Pro Ser His Thr
                5                  10                  15
Leu Asp Gln Val Asn Arg Thr His Phe Pro Phe Phe Ser Asp Val Lys
            20                  25                  30
Gly Asp His Arg Leu Val Leu Ser Val Val Glu Thr Thr Val Leu Gly
        35                  40                  45
Leu Ile Phe Val Val Ser Leu Leu Gly Asn Val Cys Ala Leu Val Leu
    50                  55                  60
Val Ala Arg Arg Arg Arg Arg Gly Ala Thr Ala Ser Leu Val Leu Asn
65                  70                  75                  80
Leu Phe Cys Ala Asp Leu Leu Phe Thr Ser Ala Ile Pro Leu Val Leu
                85                  90                  95
Val Val Arg Trp Thr Glu Ala Trp Leu Leu Gly Pro Val Val Cys His
            100                 105                 110
Leu Leu Phe Tyr Val Met Thr Met Ser Gly Ser Val Thr Ile Leu Thr
        115                 120                 125
Leu Ala Ala Val Ser Leu Glu Arg Met Val Cys Ile Val Arg Leu Arg
    130                 135                 140
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Arg Gly Leu Ser Gly Pro Gly Arg Arg Thr Gln Ala Ala Leu Leu Ala
145                 150                 155                 160
Phe Ile Trp Gly Tyr Ser Ala Leu Ala Ala Leu Pro Leu Cys Ile Leu
                165                 170                 175
Phe Arg Val Val Pro Gln Arg Leu Pro Gly Gly Asp Gln Glu Ile Pro
            180                 185                 190
Ile Cys Thr Leu Asp Trp Pro Asn Arg Ile Gly Glu Ile Ser Trp Asp
        195                 200                 205
Val Phe Phe Val Thr Leu Asn Phe Leu Val Pro Gly Leu Val Ile Val
    210                 215                 220
Ile Ser Tyr Ser Lys Ile Leu Gln Ile Thr Lys Ala Ser Arg Lys Arg
225                 230                 235                 240
Leu Thr Leu Ser Leu Ala Tyr Ser Glu Ser His Gln Ile Arg Val Ser
                245                 250                 255
Gln Gln Asp Tyr Arg Leu Phe Arg Thr Leu Phe Leu Leu Met Val Ser
            260                 265                 270
Phe Phe Ile Met Trp Ser Pro Ile Ile Ile Thr Ile Leu Leu Ile Leu
        275                 280                 285
Ile Gln Asn Phe Arg Gln Asp Leu Val Ile Trp Pro Ser Leu Phe Phe
    290                 295                 300
Trp Val Val Ala Phe Thr Phe Ala Asn Ser Ala Leu Asn Pro Ile Leu
305                 310                 315                 320
Tyr Asn Met Ser Leu Phe Arg Asn Glu Trp Arg Lys Ile Phe Cys Cys
                325                 330                 335
Phe Phe Phe Pro Glu Lys Gly Ala Ile Phe Thr Asp Thr Ser Val Arg
            340                 345                 350
Arg Asn Asp Leu Ser Val Ile Ser Ser
        355                 360
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<210> 4
<211> 1083
<212> DNA
<213> Mus musculus

<400> 4

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gtcgtggaga ccaccgttct ggggctcatc tttgtcgtct cactgctggg caacgtgtgt  180
gctctagtgc tggtggcgcg ccgtcggcgc cgtggggcga cagccagcct ggtgctcaac  240
ctctttctgcg cggatttgct cttcaccagc gccatccctc tagtgctcgt cgtgcgctgg  300
actgaggcct ggctgttggg gcccgtcgtc tgccacctgc tcttctacgt gatgacaatg  360
agcggcagcg tcacgatcct cacactggcc gcggtcagcc tggagcgcat ggtgtgcatc  420
gtgcgcctcc ggcgcggctt gagcggcccg gggcggcgga ctcaggcggc actgctggct  480
ttcatatggg gttactcggc gctcgccgcg ctgcccctct gcatcttgtt ccgcgtggtc  540
ccgcagcgcc ttcccggcgg ggaccaggaa attccgattt gcacattgga ttggcccaac  600
cgcataggag aaatctcatg ggatgtgttt tttgtgactt tgaacttcct ggtgccggga  660
ctggtcattg tgatcagtta ctccaaaatt ttacagatca cgaaagcatc gcggaagagg  720
cttacgctga gcttggcata ctctgagagc caccagatcc gagtgtccca acaagactac  780
cgactcttcc gcacgctctt cctgctcatg gtttccttct tcatcatgtg gagtcccatc  840
atcatcacca tcctcctcat cttgatccaa aacttccggc aggacctggt catctggcca  900
tccctttttct tctgggtggt ggccttcacg tttgccaact ctgccctaaa ccccatactg  960
tacaacatgt cgctgttcag gaacgaatgg aggaagattt tttgctgctt ctttttttcca 1020
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agc                                                                1083
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<210> 5
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 5

gctgtggcat gcttttaaac 20

<210> 6
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 6
cgctgtggat gtctatttgc 20

<210> 7
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 7
agttcatttc cagtaccctc catcagtggc 30

<210> 8
<211> 361
<212> PRT
<213> Rattus norvegicus

<400> 8
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1 5 10 15
Pro Asp Gln Val Asn Arg Thr His Phe Pro Phe Phe Ser Asp Val Lys
20 25 30
Gly Asp His Arg Leu Val Leu Ser Val Leu Glu Thr Thr Val Leu Gly
35 40 45
Leu Ile Phe Val Val Ser Leu Leu Gly Asn Val Cys Ala Leu Val Leu
50 55 60
Val Val Arg Arg Arg Arg Arg Gly Ala Thr Val Ser Leu Val Leu Asn
65 70 75 80
Leu Phe Cys Ala Asp Leu Leu Phe Thr Ser Ala Ile Pro Leu Val Leu
85 90 95
Val Val Arg Trp Thr Glu Ala Trp Leu Leu Gly Pro Val Val Cys His
100 105 110
Leu Leu Phe Tyr Val Met Thr Met Ser Gly Ser Val Thr Ile Leu Thr
115 120 125
Leu Ala Ala Val Ser Leu Glu Arg Met Val Cys Ile Val Arg Leu Arg
130 135 140
Arg Gly Leu Ser Gly Pro Gly Arg Arg Thr Gln Ala Ala Leu Leu Ala
145 150 155 160
Phe Ile Trp Gly Tyr Ser Ala Leu Ala Ala Leu Pro Leu Cys Ile Leu
165 170 175
Phe Arg Val Val Pro Gln Arg Leu Pro Gly Gly Asp Gln Glu Ile Pro
180 185 190
Ile Cys Thr Leu Asp Trp Pro Asn Arg Ile Gly Glu Ile Ser Trp Asp
195 200 205
Val Phe Phe Val Thr Leu Asn Phe Leu Val Pro Gly Leu Val Ile Val
210 215 220
Ile Ser Tyr Ser Lys Ile Leu Gln Ile Thr Lys Ala Ser Arg Lys Arg
225 230 235 240
Leu Thr Leu Ser Leu Ala Tyr Ser Glu Ser His Gln Ile Arg Val Ser
245 250 255
Gln Gln Asp Tyr Arg Leu Phe Arg Thr Leu Phe Leu Leu Met Val Ser
260 265 270

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Phe Phe Ile Met Trp Ser Pro Ile Ile Ile Thr Ile Leu Leu Ile Leu
        275                 280                 285
Ile Gln Asn Phe Arg Gln Asp Leu Val Ile Trp Pro Ser Leu Phe Phe
    290                 295                 300
Trp Val Val Ala Phe Thr Phe Ala Asn Ser Ala Leu Asn Pro Ile Leu
305                 310                 315                 320
Tyr Asn Met Ser Leu Phe Arg Ser Glu Trp Arg Lys Ile Phe Cys Cys
                325                 330                 335
Phe Phe Phe Pro Glu Lys Gly Ala Ile Phe Thr Glu Thr Ser Ile Arg
            340                 345                 350
Arg Asn Asp Leu Ser Val Ile Ser Thr
        355                 360

<210> 9
<211> 1083
<212> DNA
<213> Rattus norvegicus

<400> 9
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gtcctggaga ccaccgttct gggactcatc tttgtggtct cactgctggg caacgtgtgt   180
gccctggtgc tggtggtgcg ccgtcggcgc cgtggggcga cagtcagctt ggtgctcaac   240
ctcttctgcg cggatttgct cttcaccagc gccatccctc tagtgctcgt ggtgcgctgg   300
actgaagcct ggctgctggg gcccgtcgtc tgccacctgc tcttctacgt gatgaccatg   360
agcggcagcg tcacgatcct cacgctggcc gcggtcagcc tggagcgcat ggtgtgcatc   420
gtgcgcctgc ggcgccggctt gagcggcccg gggcggcgga cgcaggcggc gctgctggct   480
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ccgcagcgcc ttcccggcgg ggaccaggaa attccgattt gcacattgga ttggcccaac   600
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cttacgctga gcttggcata ctccgagagc caccagatcc gagtgtccca gcaggactac   780
cggctcttcc gaacgctctt cctgctcatg gtttccttct tcatcatgtg gagtcccatc   840
atcatcacca tcctcctcat cttgatccag aacttccggc aggacctggt tatctggccg   900
tccctttttct tctgggtggt ggccttcacg tttgccaact ccgccctaaa ccccattctg   960
tacaacatgt cgctgttcag gagcgagtgg aggaagattt tttgctgctt ctttttccca  1020
gagaagggag ccatttttac agaaacgtct atcaggcgaa atgacttgtc tgttatttcc  1080
acc                                                                1083

<210> 10
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 10
gtggtggcct tcacgtttg                    19

<210> 11
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 11
cgctcctgaa cagcgacat                    19

<210> 12
<211> 26
<212> DNA
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<213> Artificial Sequence

<220>
<223> probe

<400> 12
caactccgcc ctaaacccca ttctgt 26

<210> 13
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 13
gtcgacatgt cccctgagtg tgcgcagacg acg 33

<210> 14
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 14
gctagcttag gtggaaataa cagacaagtc att 33

<210> 15
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 15
tccgagtgtc ccaacaagac tac 23

<210> 16
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 16
gactccacat gatgaagaag gaaa 24

<210> 17
<211> 22
<212> DNA
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<220>
<223> probe

<400> 17
ccgcacgctc ttcctgctca tg 22

<210> 18

<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 18
gtggtggcct tcacgtttg 19

<210> 19
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 19
cgctcctgaa cagcgacat 19

<210> 20
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> probe

<400> 20
caactccgcc ctaaacccca ttctgt 26

<210> 21
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> base sequence of the sense strand of siRNA m14i561

<220>
<221> misc_DNA
<222> (20)..(21)
<223> n stands for deoxy thymidine

<400> 21
ggaccaggaa auuccgauun n 21

<210> 22
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> base sequence of the antisense strand of siRNA m14i561

<220>
<221> misc_DNA
<222> (1)..(2)
<223> n stands for deoxy thymidine

<400> 22
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